REMARKS

Claims 1-30 are pending. The claims have been amended without disclaimer or prejudice. Support for the amendments is found *inter alia* in the original claims. Amended claim 1 further finds support in the specification at page 10 paragraphs [0048] and [0049]. Claim 4 has been amended without prejudice or disclaimer to recite the elected element. No new matter has been added.

The amendment to the specification finds support at pages 56 and 57 paragraphs [00235] to [00238]. No new matter has been added.

Election/Restriction

The Examiner asserts that newly added claims 27-30 belong to non-elected Group VII. Applicants respectfully disagree and traverse at least for claims 27 and 28. In the Restriction Requirement (Official Action mailed March 22, 2006, page 2), the Examiner stated that the claims of Group VII, claims 12-13, were drawn to a method for removing a DNA sequence from chromosomal DNA of a eukaryotic cell. Claims 27 and 28 depend from claims 2 and 1, respectively, and are drawn to recombination systems. Group I was characterized in the Restriction Requirement as claims 2-4, drawn to a recombination system. Claims 27 and 28 are not drawn to a method, but rather to a recombination system. Thus, Applicants respectfully submit that claims 27 and 28 should be included in Group I or at least be considered as being linked with linking claim 1. Reconsideration and withdrawal of the restriction to requirement at least to claims 27 and 28 is respectfully requested.

Objections to the Specification

The Examiner requested that the brief description of Figure 7 be amended to include the labels associated with the multiple views. In light of the amendment, the objection is believed to be rendered moot. Reconsideration and withdrawal of the objection is respectfully requested.

Rejections under 35 U.S.C. § 112, second paragraph

Claims 1-4 were rejected under 35 U.S.C. § 112, second paragraph, for indefiniteness.

In the present amendment, the claims have been amended to address the rejections under 35 U.S.C. § 112, second paragraph. Reconsideration and withdrawal of the rejections is requested.

Rejections under 35 U.S.C. § 102

Claims 1-4 were rejected under 35 U.S.C. § 102(b) as being anticipated by Lyznik et al. (hereinafter "Lyznik").

The Examiner alleges that Lyznik meets all the limitations of claims 1-4 by teaching a recombination system which comprises in a 5' to 3' orientation an intron sequence of *Ubi-I* gene, a selection marker, a recognition sequence for site-directed induction of DNA double-strand breaks, i.e. the FRTm site, another intron, a FRT site and another vector for the FLP recombinase. The Examiner characterizes the first intron of the *Ubi-I* gene as corresponding to homology sequence A and the second intron as corresponding to homology sequence B of claim 1 of the present application. The Examiner also states that the FLP recombinase corresponds to the enzyme that makes the double strand break at the FRT and FRTm sites. Applicants respectfully disagree with the Examiner's characterizations of the Lyznik reference and the present invention and traverse the rejection.

The Examiner points to Figure 1 for a description of the binary vector of Lyznik. In the construct described in Figure 1 of Lyznik, the FRT recognition site is outside the intron sequence of *Ubi-I* gene which the Examiner alleged as corresponding to homology sequence A. Claim 1 of the present application recites that the recognition sequence for site-directed induction of double-stranded breaks is found between homology sequences A and B, not outside as in Lyznik. Furthermore, the Examiner acknowledged that the FLP recombinase of Lyznik makes double strand breaks between the FRT and FRTm sites. Rather claim 1 of the present application recites that the enzyme is suitable for inducing breaks at a recognition sequence, which sequence is between the homology sequences.

Moreover, the product of the site-specific recombination reaction in Lyznik contains a chimeric FRT originating from the recombination of the FRT and FRTm recognition sites (see Lyznik, Figures 1 and 4, and at page 3787, left column second paragraph). Claim 1 of the

present application recites that the homology sequences A and B are such that they allow for homology recombination between homology sequences A and B. As recited in the specification at page 9 paragraph [0040], "[t]he sequences which are deleted are those located between the homology sequences A and B." Contrary to the teaching of Lyznik, the present invention describes a method in which the recognition sites are deleted as the result of the homologous recombination event.

Therefore, Lyznik does not teach or disclose the method as claimed and thus does not anticipate the claims. Reconsideration and withdrawal of the rejection is respectfully requested.

In addition, claims 1-4 were rejected under 35 U.S.C. § 102(e) as being anticipated by Dujon et al. (hereinafter "Dujon").

The Examiner alleges that Dujon meets all the limitations of claims 1-4 by teaching a recombination system which comprises in a 5' to 3' orientation a LTR sequence, a I-SceI type II restriction enzyme recognition site as a recognition sequence for site-directed induction of DNA double-strand breaks, a selection marker, another LTR sequence and I-SceI type II restriction enzyme recognition site, and additionally a second vector expressing I-SceI type II restriction enzyme. The Examiner also alleges that the two LTR sequences meet the structural limitations for homology sequences A and B of the claims. Applicants respectfully disagree and traverse the rejection.

The brief description of Figure 25 discloses that the LTRs each contain an I-Sce I recognition site and a PhleoLacZ gene (see Dujon, column 7, lines 1-23). The brief description of Figure 25 also discloses several times that the recognition sequence is located within the LTR regions, rather than between homology sequences as required by the present claims. Thus the endonuclease of Dujon cuts within the homology sequence, not in between the homology sequences as in the present invention. If more than one I-Sce I site is cut, no homology region is even available. Furthermore, the end joining described in Figure 25 B3 of Dujon only repairs the ends and the resulting recombination product results in a solitary LTR, not homologous recombination of the homology sequences as in the present invention.

Therefore, Dujon does not teach or disclose the method as claimed and thus does not anticipate the claims. Reconsideration and withdrawal of the rejection is respectfully requested.

CONCLUSION

For at least the above reasons, Applicants respectfully request withdrawal of the rejections and allowance of the claims.

Accompanying this response is a petition for a three-month extension of time to and including January 17, 2007 to respond to the Office Action mailed July 17, 2006 with the required fee authorization. No further fees are believed due. If any additional fee is due, please charge our Deposit Account No. 03-2775, under Order No. 13173-00010-US from which the undersigned is authorized to draw.

Respectfully submitted,

By

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